Amendments to the Claims

10. (Currently amended) A method of reducing excess heme in an ~~an *in vivo* or *in*~~ *vitro* system comprising

a) administering to the system an amount of an apoprotein composition sufficient to reduce the excess heme, the apoprotein composition comprising an alpha or beta globin-like protein comprising at least one mutation consisting of a single amino acid change that stabilizes heme binding.

11. (Original) The method of claim 10, wherein the mutation in the globin-like protein is at an amino acid position in either the alpha or beta subunit of hemoglobin selected from the group consisting of B10, CD3, E11, and G8.

12. (Original) The method of claim 11, wherein the mutation in the globin-like protein is a mutation in either the alpha or beta subunit of hemoglobin selected from the group consisting of B10→ Phe, B10→ Val, B10→ Ile, CD3→ His, E11→ Leu, E11→ Trp, E11→ Phe, and G8→ Ile.

13. (Original) The method of claim 12, wherein the mutation is selected from the group consisting of:

(a) Leu28(B10) → Val in beta globin;
(b) Leu28(B10) → Ile in beta globin;
(c) Ser44(CD3) → His in beta globin;
(d) Leu29(B10) → Phe in alpha globin;
(e) Val67(E11) → Trp in beta globin;
(f) Val62(E11) → Phe in alpha globin;
(g) Val67(E11) → Phe in beta globin;
(h) Leu106(G8) → Ile in beta globin; and
(i) Val62(E11) → Leu in alpha globin.

14. (Original) The method of claim 10, wherein the mutation in the globin-like protein is at an amino acid position in the alpha or beta subunit selected from the group consisting of E7 and B13.

15. (Original) The method of claim 14, wherein the mutation in the alpha or beta globin-like protein is selected from the group consisting of E7→ Leu, E7→ Phe, E7→ Met, E7→ Trp, B13→ Leu, B13→ Phe, B13→ Met, and B13→ Trp.

16. (New) A method of reducing excess heme in a system comprising:

administering to the system an amount of an apoprotein composition sufficient to reduce the excess heme, the apoprotein composition comprising an alpha or beta globin-like protein comprising at least one mutation consisting of a single amino acid change that stabilizes heme binding.